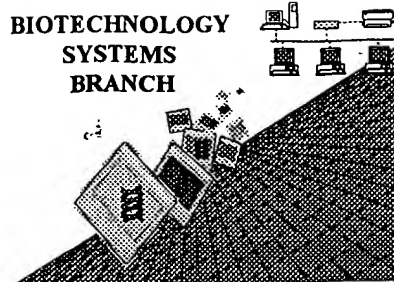# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/895,913_

Source: _OIPE_

Date Processed by STIC: _7/23/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,913   TIME: 13:44:58

Input Set : A:\06132.013001.seqlist.txt
Output Set: N:\CRF3\07232001\I895913.raw

Does Not Comply
Corrected Diskette Needed

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 4 <110> APPLICANT: Kleanthous, Harold
 5         Al-Garawi, Amal
 6         Miller, Charles
 7         Tomb, Jean Francois
 8         Oomen, Raymond P.
10 <120> TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES
11         ENCODING NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER
12         GENOME
14 <130> FILE REFERENCE: 06132/043001
16 <140> CURRENT APPLICATION NUMBER: US/09/895,913
17 <141> CURRENT FILING DATE: 2001-06-29
19 <160> NUMBER OF SEQ ID NOS: 368
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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ERRORED SEQUENCES

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1161 <210> SEQ ID NO: 12
1162 <211> LENGTH: 1844              pp 4-6
1163 <212> TYPE: PRT
1164 <213> ORGANISM: Helicobacter pylori
1166 <400> SEQUENCE: 12
1167 Leu Leu Gly Thr Met Met Met Met Leu Phe Gln Gln Asn Leu Trp Trp
1168  1           5                   10                  15
1169 Phe Asn Asn Ile Met Val Val Glu Gln Gly Gly Ser Ile Ile Ile Ile
1170             20                  25                  30
1171 Ile Ser Gly Thr Pro Pro Phe Val Gln Gln His Pro Lys Lys Thr Ala
1172         35                  40                  45
1173 Ala Lys Phe Val Val Val Val Val Glu Glu Glu Phe Ser Ser Ala Leu
1174     50                  55                  60
1175 Ser Ser Tyr Lys Lys Phe His Tyr Tyr Ile Leu Arg Arg Arg Arg Phe
1176 65                  70                  75                  80
1177 Ser Thr Thr Asp Ala Asp Asp Gly Gly Phe Gly Val Val Val Arg Lys
1178             85                  90                  95
1179 Lys Ile His Ser Arg Arg Lys Pro Pro Val Cys Val Val Arg Val Leu
1180             100                 105                 110
1181 Leu Ser Arg Arg Tyr Lys Asn Asn Asn Asn Asn Asp Leu Leu Trp Leu
1182         115                 120                 125
1183 Leu Leu Arg Arg Ser Leu Leu Leu Trp Gly Gly Arg Trp Gly Leu Cys
1184         130                 135                 140
1185 Cys Leu Gly Ser Ser Ser Arg Arg Lys Pro Ile Ile Asn Gly Gly Gly
1186 145                 150                 155                 160
1187 Asp Leu Leu Leu Leu Leu Trp Glu Glu Ile Cys Cys Tyr Leu His His
1188             165                 170                 175
1189 Gln Phe Gln Gln Arg Leu Leu Ile Phe Leu Leu Leu Leu Leu Asn Asn
1190         180                 185                 190
1191 Asn Cys Arg Arg Thr Leu Thr Thr Gly Gly Gly Gly Asp Asp Asp Ile
```

```
1192            195                 200                 205
1193   Leu Thr Thr Thr Thr Leu Met Lys Lys Leu Asn Ala Ala Arg Val Val
1194       210                 215                 220
1195   Ile Thr Arg Arg Phe Gln Thr Thr Gly Phe Phe Phe Phe Phe Leu Thr
1196   225                 230                 235                 240
1197   Asn Asn Val Arg Arg Gln His Ser Ser Gly Glu Phe Phe Ile Pro Pro
1198                   245                 250                 255
1199   Leu Ser Met Met Met Met Met Ile Lys Lys Phe Leu Leu Gly Ile Ser
1200                   260                 265                 270
1201   Ser Trp Gly Gly Leu Phe Phe Ile Gln Gly Gly Gly Gly Val Ser Leu
1202                   275                 280                 285
1203   Leu Glu Asn Thr Thr Phe Ala Gly Pro Pro Ile Asn Gly Gly Asp Arg
1204       290                 295                 300
1205   Leu Ile Ile Met Met Val Ala Ala Tyr Gly Phe Phe Tyr Phe Phe Asn
1206   305                 310                 315                 320
1207   Ser Ile Ile Ile Ile Ile Gly Gly Gly His Ser Leu Leu Ile Lys Lys
1208                   325                 330                 335
1209   Asn Asn Asn Tyr Phe Gln Gln Thr Leu Lys Lys Lys Lys Trp Leu Leu
1210                   340                 345                 350
1211   Leu Val Ser Lys Lys Cys Glu Glu Ser His His His Asn Gly Asn Asn
1212               355                 360                 365
1213   Tyr Phe Phe Phe Phe Phe Phe Gln Gln Phe Gln Gln Lys Pro Asn Asn
1214       370                 375                 380
1215   Gly Tyr Leu Gly Gly Ser Gln Thr Thr Thr Thr Thr Thr Ala Ala Arg
1216   385                 390                 395                 400
1217   Lys Arg Arg Gln Ala Phe Phe Phe Tyr Tyr Gln Gln Arg Arg Arg Ile
1218               405                 410                 415
1219   Leu Leu Leu Leu Thr Ala Gln Gln Ala Phe Asn Asn Gly Val Val Ile
1220               420                 425                 430
1221   Ile Ile Asn Pro Asn Asn Ser Ser Ser Ser Ser Ser Leu Gln Ser Ser
1222               435                 440                 445
1223   Ile Ile Asn Asn Ala Ala Cys Asn Phe Phe Met Ala Ala Pro Leu Phe
1224       450                 455                 460
1225   Phe Phe Phe Phe Lys Thr Thr Phe Trp Trp Thr Leu His His Leu Ile
1226   465                 470                 475                 480
1227   Ile Phe Gln Arg Arg Ile Arg Ile Ile Ile Ile Leu Ile Lys Lys Thr
1228               485                 490                 495
1229   Leu Asn Asn Lys Gly Gly Lys Ile Ser Ser Ile Asn Phe Phe Arg Arg
1230               500                 505                 510
1231   Arg Arg Arg Arg Tyr Phe Lys Thr Thr Thr Met Asn Asn Ser Lys Lys
1232               515                 520                 525
1233   Pro Lys Lys Ser Phe Asn Asn Asn Asn Asn Leu Lys Lys Gly Arg Gly
1234       530                 535                 540
1235   Gly Arg Ile Ser Ser Leu Asn Asn Leu Lys Leu Leu Ile Ser Ser Ser
1236   545                 550                 555                 560
1237   Ser Met Ala Ile Ile Val Phe Asn Asn Ser Cys Cys Val Phe Met Met
1238               565                 570                 575
1239   Asn His Ser Ser Asn Phe Phe Phe Phe Phe His Ile Ile Arg Leu Leu
1240               580                 585                 590
```

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1241  Asn Ser Asp Asp Phe Phe Ala Ala Asn Ser Thr Thr Thr Thr Thr Asn
1242      595             600             605
1243  Phe Phe Lys Arg Ser Ser Met Val Val Leu Asn Asn Phe Arg Gln Gln
1244      610             615             620
1245  Ala Val Thr Thr Thr Thr Ile Arg Arg Asn Ala Lys Lys Glu Phe Phe
1246  625             630             635             640
1247  Val Leu Gly Gly Lys Gly Ile Ile Glu Ser Ser Ser Ser Ser Leu Tyr
1248              645             650             655
1249  Glu Glu Tyr Leu Leu Gly Asp Lys Lys Asn Phe Arg Arg Met Met Met
1250          660             665             670
1251  Leu Gln Ala Ala Ala Ala Ala Asn Ile Ile Trp Leu Asn Asn Gly Ile
1252          675             680             685
1253  Thr Thr Tyr Glu Glu Asp Pro Phe Phe Met Ala Tyr Tyr Tyr Tyr Arg
1254      690             695             700
1255  Leu Thr Thr Ala Asp Tyr Tyr Val Thr Ala Phe Phe Ser Trp Arg Arg
1256  705             710             715             720
1257  His Ala Gln Tyr Tyr Leu Lys Lys Ile Thr Glu Glu Leu Ala Thr Ala
1258              725             730             735
1259  Ala Lys Val Gln Gln Gln Gln Gln Ser Gln Gln Arg Arg Phe Phe Ile
1260          740             745             750
1261  Ile Arg Arg Phe Asn Asn Arg Ser Cys Met Ile Ile Ile Ile Thr Lys
1262          755             760             765
1263  Lys Lys Pro Tyr Asn Asn Asn Arg Arg Ile Pro Ile Ile Tyr Thr Ser
1264          770             775             780
1265  Ser Gly Gly Gly Gly Gly His Leu Leu Leu Arg Arg Asn Ile Lys Lys
1266  785             790             795             800
1267  Leu Ser Ser Thr Ile Ile Thr Pro Gly Gly Gly Gly Gly Tyr Asn Asn
1268              805             810             815
1269  Ala Lys Pro Pro Pro Tyr Lys Lys Leu His His Leu Gln Ser Ser Leu
1270          820             825             830
1271  Ser Leu Leu Leu Leu Ser Lys Ile Ile Asn Met Ile Ile Gln Phe Phe
1272          835             840             845
1273  Val Arg Ser Ser Leu Pro Lys Lys Ser Gln Gln Gln Gln Gln Phe Ile
1274      850             855             860
1275  Phe Phe Gly Leu Leu Asp Asn Leu Leu Pro Glu Glu Val Leu Leu Thr
1276  865             870             875             880
1277  Leu Phe Phe Phe Phe Phe Ile Phe Phe Lys Val Trp Trp Ser Leu Gln
1278              885             890             895
1279  Glu Glu Leu Glu Glu Glu Tyr Arg Arg Arg Arg Leu Ser Ile Ile Phe
1280          900             905             910
1281  Ser Asn Asn Asn Met Ile Ser Ser Gln Gly Asn Asn Arg Cys Cys Cys
1282          915             920             925
1283  Cys Cys Ser Asp Gln Gln Arg Gly Gly Thr Asn Thr Thr Lys Arg Gly
1284      930             935             940
1285  Gly Gly Leu Leu Gly Glu Gly Gly Gly Gly Gly Lys Glu Glu Met Cys
1286  945             950             955             960
1287  Gly Gly Gly Ile Thr Thr Cys Gln Gln Val Gln Thr Thr Leu Ile Gly
1288              965             970             975
1289  Asn Cys Cys His Ser Ser Ser Ala Leu Leu Ala Thr Thr Asn Ala Asn
```

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       1290           980              985              990
       1291 Asn Gly Gly Gly Gly Gly Lys His Leu Leu Leu Pro Pro Thr Ile Gly
       1292      995             1000             1005
       1293 Gly Arg Glu Arg Arg Gly Gly Gly Gly Gly Ser Ser Ser Ser Ser Asn
       1294     1010            1015             1020
       1295 Val Val Phe Lys Lys Ala Leu Ile Ile Val Leu Leu Ser Ser Leu Thr
E--> 1296 1025            1030             1035           (104)1040
       1297 Leu Leu Leu Leu Lys Gly Pro Pro Lys Ile Phe Phe Leu Leu Leu Gly
       1298             1045             1050             1055
       1299 Lys Gly Gly Ile Glu Lys Lys Phe Trp Trp Trp Trp Trp Lys Arg Phe
       1300             1060             1065             1070
       1301 Phe Gly Met Met Leu Ser Asn Asn His Leu Arg Ala Ala Asn Asp Asn
       1302        1075             1080             1085
       1303 Asn Asn Asn Asn Ile Pro Pro Arg Phe Ser Ser Thr Ser Ser Lys Asp
       1304     1090             1095             1100
       1305 Asp Trp Ile Leu Ala Ala Ala Ala His Cys Leu Leu Pro Thr Glu Glu
E--> 1306 1105            1110             1115           (112)
       1307 Glu Ser Ala Ala Ser Ala Phe Phe Lys Arg Arg Arg Arg Arg His Gly
       1308             1125             1130             1135
       1309 Asn Asn Ile Ile Lys Thr Val Val Arg Cys Phe Phe Val Lys Lys Gly
       1310        1140             1145             1150
       1311 Leu Leu Leu Leu Leu Leu Ala Leu Leu Ser Tyr Gly Gly Glu Lys Lys
       1312        1155             1160             1165
       1313 Lys Asp Gln Gln Ala Phe Arg Arg Lys Ser Lys Lys Lys Lys Pro Ile
       1314     1170             1175             1180
       1315 Leu Leu Gly Phe Glu Glu Ile His His Lys Leu Leu Gly Ile Glu Glu
E--> 1316 1185            1190             1195           (120)
       1317 Cys Arg Arg Arg Arg Arg Phe His Gln Gln Thr Gly Gly Gly Lys Gln
       1318             1205             1210             1215
       1319 Gln Leu Glu Phe Phe Leu Pro Pro Asn Phe Val Val Val Val Val Gly
       1320        1220             1225             1230
       1321 Gly Gly Glu Ser Ser Ser Leu Ile Lys Lys Gly Ser Ser Leu Cys Cys
       1322        1235             1240             1245
       1323 Lys Thr Tyr Tyr Tyr Tyr Arg Thr Ser Ser Asp Lys Thr Thr Phe Trp
       1324     1250             1255             1260
       1325 Trp Ile Phe Gln Met Ile Ile Thr Ser Ser Ser Ser Ser Leu Asn Gln
E--> 1326 1265            1270             1275           (128)
       1327 Gln Asn Ser Ser Ser Trp Leu Leu Ser Ala Gly Gly Ala Ala Leu Val
       1328             1285             1290             1295
       1329 Asn Asn Asn Asn Asn Ala Leu Leu His His His Thr Leu Val Val Glu
       1330             1300             1305             1310
       1331 Leu Leu His His His Leu Ala Val Lys Lys Lys Leu Asn Asp Asp Ile
       1332        1315             1320             1325
       1333 Arg Arg Met Ala Asn Lys Ile Ile Glu Gln Gln Gln Gln Gln Ser Leu
       1334     1330             1335             1340
       1335 Arg Arg Lys Asn Lys Ile Ile Cys Ala Leu Leu Gly Val Tyr Tyr Tyr
E--> 1336 1345            1350             1355           (136)
       1337 Tyr Tyr Gln Gly Gly Arg Leu His His Cys Leu Asn Asn Leu Gln Gln
       1338             1365             1370             1375
```

[Handwritten marginal note:] When numbering the last amino acid on a line, please end the number directly under the last letter of the amino acid e.g. Thr 1040

```
     1339  Ile Glu Glu Asn Trp Ala Ala Ala Ala Trp Ala Leu Leu Leu Gly Ser
     1340              1380              1385              1390
     1341  Ser Gly Val Val Thr Ile Phe Phe Gln Arg Gly Gly Phe Gln Gln Gln
     1342           1395              1400              1405
     1343  Gln Gln Cys Gly Ile Ile Ile Phe Thr Asn Asn Gln Leu Val Val Val
     1344        1410              1415              1420
     1345  Thr Thr Thr Gly Gly Gly Gly Gly Gly Leu Asn Asn Cys Gly Gly Gly
E--> 1346  1425              1430              1435              144
     1347  Ser Leu Leu Leu Phe Asn Asn Glu Lys Tyr Tyr Ser Ile Ser Ser Ser
     1348              1445              1450              1455
     1349  Ser Arg Ser Ile Ile Gly Lys Leu Leu Val Tyr Tyr Leu Lys Ile Ile
     1350              1460              1465              1470
     1351  Ser Asn Ile Ile Ile Arg Arg Arg Arg Arg Leu Lys Arg Arg Leu Thr
     1352              1475              1480              1485
     1353  Thr Leu Thr Leu Leu Cys Ser Met Thr Thr Ser Val Gln Gln Gln Gln
     1354        1490              1495              1500
     1355  Gln Gly Gln Gln Leu Arg Glu Glu Phe Ile Ile Met Gly Gly Glu Lys
E--> 1356  1505              1510              1515              152
     1357  Ser Ser Ile Leu Gln Gln Gln Gln Ala Arg Gln Gln Pro Thr Asn Asn
     1358              1525              1530              1535
     1359  Asn Thr Thr Lys Arg Met Met Asn Asn Phe Phe Phe Phe Phe Phe Phe
     1360           1540              1545              1550
     1361  Phe Cys Asn Leu Met Met Leu Val Asp Asp Phe Lys Ser Ser Tyr Lys
     1362        1555              1560              1565
     1363  Lys Thr Thr Ile Ile Ile Ile Ile Thr Leu Leu Phe Arg Ala Ala Thr
     1364        1570              1575              1580
     1365  Leu Leu Leu Lys Ala Ala Ser Phe Asp Asp Ile Thr Thr Thr Thr Leu
E--> 1366  1585              1590              1595              160
     1367  Leu Thr Thr Asn Ser Asn Asn Gln Gly Gly Ile Leu Ala Ala Asn Leu
     1368              1605              1610              1615
     1369  Asn Asn Gly Ser Gly Ser Ser Ala Arg Arg Glu Asn Gly Gly Glu Cys
     1370           1620              1625              1630
     1371  Gly Gly Ala Ile Ile Lys Ser Glu Glu Glu Glu Glu Ser Leu Leu Leu
     1372        1635              1640              1645
     1373  Ser Ser Thr Ile Lys Lys Asn Gln Gln Asp Tyr Trp Leu Ala Ala Ala
     1374        1650              1655              1660
     1375  Ala Ile Leu Arg Arg Met Ser Tyr Tyr Gln Ser Ser Leu Ser Ser Phe
E--> 1376  1665              1670              1675              168
     1377  Asn Thr Thr Thr Gln Gln Gln Gln Gln Arg Arg Leu Leu Arg Leu Leu
     1378              1685              1690              1695
     1379  Asn Ala Lys Lys His Ala Leu Leu Val Met Met Asn Gln Ile Ile Ile
     1380           1700              1705              1710
     1381  Ile Ile Arg Gly Gly Glu Leu Glu Glu Ile Thr Ser Ser Leu Tyr Tyr
     1382           1715              1720              1725
     1383  Pro His Leu Thr Ala Ala Ala Ala Asn Ala Cys Cys Leu Asn Gly Gly
     1384        1730              1735              1740
     1385  Phe Thr Thr Ala Met Thr Thr Gln Pro Val Val Tyr Trp Gly Ser Ser
E--> 1386  1745              1750              1755              176
     1387  Trp Phe Lys Asp Asp Ser Gly Ala Ala Trp Cys Cys Ser Ser Ile Ile
```

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     1388                    1765            1770            1775
     1389  Ile Ile Ile Tyr Asp Asp Ser Ser Ser Ser Ala Ser Leu Leu Lys Pro
     1390            1780            1785            1790
    .1391  Pro Gly Tyr Ser Ser Pro Leu Val Val Val Trp Ser Ile Ile Ile
     1392        1795            1800            1805
     1393  Lys Tyr Tyr Ser Arg Arg Val Leu Val Val Asp Ala Ile Ile Ile Cys
     1394      1810            1815            1820
     1395  Cys Cys Cys Cys Gln Phe Phe Phe Cys Cys Leu Asn Glu Glu Phe Cys
E--> 1396  1825                1830            1835            184
     1397  Gly Gly Lys Gly
     1463  <210> SEQ ID NO: 14
     1464  <211> LENGTH: 189
     1465  <212> TYPE: PRT
     1466  <213> ORGANISM: Helicobacter pylori
     1468  <400> SEQUENCE: 14
     1469  Met Ile Asn Arg Ala Thr Leu His Asn Tyr Ser Glu Ile Glu Lys Lys
     1470  1                 5                 10              15
     1471  Asn Ile Met Leu Ser Asp Arg Val Val Val Ile Arg Ser Gly Asp Val
     1472            20              25              30
     1473  Ile Pro Lys Ile Ile Lys Pro Leu Glu Ser Tyr Arg Asp Gly Ser Gln
     1474          35              40              45
     1475  His Lys Ile Glu Arg Pro Lys Val Cys Pro Ile Cys Ser His Glu Leu
     1476      50              55              60
     1477  Leu Cys Glu Glu Ile Phe Thr Tyr Cys Gln Asn Leu Asn Cys Pro Ala
     1478  65              70              75              80
     1479  Arg Leu Lys Glu Ser Leu Ile His Phe Ala Ser Lys Asp Ala Leu Asn
     1480            85              90              95
     1481  Ile Gln Gly Leu Gly Asp Lys Val Ile Glu Gln Leu Phe Glu Glu Lys
     1482          100             105             110
     1483  Leu Ile Phe Asn Ala Leu Asp Leu Tyr Ala Leu Lys Leu Glu Asp Leu
     1484          115             120             125
     1485  Met Arg Leu Asp Lys Phe Lys Ile Lys Lys Ala Gln Asn Leu Leu Asp
     1486      130             135             140
     1487  Ala Ile Leu Lys Ser Lys Asn Pro Pro Leu Trp Arg Leu Ile Asn Ala
     1488  145             150             155             160
     1489  Leu Gly Ile Glu His Ile Gly Lys Gly Ala Ser Lys Thr Leu Ala Lys
     1490            165             170             175
E--> 1491  Tyr Gly Leu Asn Val Leu Glu Lys Ser Glu Xaa Ser Phe
     1492            180             185
     2771  <210> SEQ ID NO: 34
     2772  <211> LENGTH: 454
     2773  <212> TYPE: PRT
     2774  <213> ORGANISM: Helicobacter pylori
     2776  <400> SEQUENCE: 34
     2777  Met Phe Leu Leu Arg His Leu Thr Ser Ala Cys Val Phe Leu Ala Ser
     2778  1                 5                 10              15
     2779  Lys Cys Leu Pro Asp Ser Phe Val Leu Val Ala Leu Leu Ser Phe Val
     2780            20              25              30
     2781  Val Phe Val Leu Val Tyr Cys Leu Thr Gly Gln Asp Ala Phe Ser Val
```

same

see item 9 on Error summary sheet

p. 7

```
2782            35                    40                    45
2783  Ile Ser Ser Trp Gly Asn Gly Ala Trp Thr Leu Leu Gly Phe Ser Met
2784      50                    55                    60
2785  Gln Met Ala Leu Ile Leu Val Leu Gly Gln Ala Leu Ala Asn Ala Lys
2786  65                    70                    75                    80
2787  Leu Val Gln Lys Leu Leu Lys Tyr Leu Ala Ser Leu Pro Lys Gly Tyr
2788                85                    90                    95
2789  Tyr Thr Ala Leu Trp Leu Val Thr Phe Leu Ser Leu Ile Ala Asn Trp
2790                100                   105                   110
2791  Ile Asn Trp Gly Phe Gly Leu Val Ile Ser Ala Ile Phe Ala Lys Glu
2792                115                   120                   125
2793  Ile Ala Lys Asn Val Lys Gly Val Asp Tyr Arg Leu Leu Ile Ala Ser
2794          130                   135                   140
2795  Ala Tyr Ser Gly Phe Val Ile Trp His Gly Gly Leu Ser Gly Ser Ile
2796  145                   150                   155                   160
2797  Pro Leu Ser Val Ala Thr Gln Asn Glu Asn Leu Ser Lys Ile Ser Ala
2798                165                   170                   175
2799  Gly Val Ile Glu Lys Ala Ile Pro Ile Ser Gln Thr Ile Phe Ser Ser
2800                180                   185                   190
2801  Tyr Asn Leu Ile Ile Ile Gly Ile Ile Leu Val Gly Leu Pro Phe Leu
2802                195                   200                   205
2803  Met Ala Met Ile His Pro Lys Lys Glu Glu Ile Val Glu Ile Asp Ser
2804          210                   215                   220
2805  Lys Leu Leu Lys Asp Glu Tyr Lys Glu Ile Glu Leu Ile Ser His Gln
2806  225                   230                   235                   240
2807  Gln Asp Lys Thr Ile Ala His Phe Leu Glu Asn Ser Ala Leu Leu Ser
2808                245                   250                   255
2809  Tyr Leu Leu Val Phe Leu Gly Phe Gly Tyr Leu Gly Val Tyr Phe Phe
2810                260                   265                   270
2811  Lys Gly Gly Gly Ile Ser Leu Asn Ile Val Asn Thr Ile Phe Leu Phe
2812                275                   280                   285
2813  Leu Gly Ile Leu Leu His Lys Thr Pro Leu Ala Tyr Val Lys Ala Ile
2814          290                   295                   300
2815  Asp Arg Ser Ala Xaa Ser Val Ala Gly Ile Leu Leu Gln Phe Pro Phe
2816  305                   310                   315                   320
2817  Tyr Ala Gly Ile Met Gly Met Met Ala Ser His Ser Val Gly Gly His
2818                325                   330                   335
2819  Ser Leu Ala Gln Met Leu Ser Leu Ala Phe Thr His Ile Ala Asn Glu
2820                340                   345                   350
2821  Lys Thr Phe Val Leu Met Thr Phe Leu Ser Ala Gly Ile Val Asn Ile
2822                355                   360                   365
2823  Phe Ile Pro Ser Gly Gly Gly Gln Trp Ala Ile Gln Ala Pro Ile Met
2824          370                   375                   380
2825  Leu Pro Ala Gly Gln Ser Leu Gly Val Asp Pro Gly Val Val Ser Met
2826  385                   390                   395                   400
2827  Ala Ile Ala Trp Gly Asp Ala Trp Thr Asn Met Ile Gln Pro Phe Trp
2828                405                   410                   415
2829  Ala Leu Pro Ala Leu Ala Ile Ala Gly Leu Gly Ala Lys Asp Ile Met
2830          420                   425                   430
```

E--> 2815

see item 9

```
2831  Gly Tyr Cys Val Leu Thr Leu Ile Phe Val Gly Leu Val Val Cys Gly
2832          435             440             445
2833  Val Phe Tyr Phe Leu Val
2834      450
9641  <210> SEQ ID NO: 146
9642  <211> LENGTH: 435
9643  <212> TYPE: PRT
9644  <213> ORGANISM: Helicobacter pylori
9646  <400> SEQUENCE: 146
9647  Met Gly Phe Phe Lys Leu Lys Glu His Asn Thr Asn Ile Ala Thr Glu
9648  1               5               10              15
9649  Phe Arg Ala Gly Leu Thr Thr Phe Ile Thr Met Ile Tyr Ile Val Pro
9650          20              25              30
9651  Leu Asn Ala Leu Ile Leu Ser Gln Ala Asn Met Pro Tyr Glu Ala Leu
9652          35              40              45
9653  Leu Ser Ala Thr Ala Ile Ile Thr Ile Leu Ser Ser Val Phe Asn Gly
9654      50              55              60
9655  Leu Trp Ala Asn Thr Pro Ile Ala Met Ser Val Gly Leu Gly Leu Ser
9656  65              70              75              80
9657  Ala Tyr Phe Ser Phe Gly Leu Val Gln Gly Leu Lys Leu Pro Trp Gln
9658              85              90              95
9659  Ser Ala Leu Gly Ile Val Ala Leu Ser Gly Ala Ile Phe Val Ile Leu
9660          100             105             110
9661  Ser Phe Thr Lys Phe Arg Ser Trp Val Met Arg Ser Ile Pro Ser Asp
9662          115             120             125
9663  Leu Arg Arg Ala Val Ser Ala Gly Ile Gly Ala Phe Ile Ala Phe Ile
9664          130             135             146
9665  Gly Leu Lys Glu Met His Ile Val Val Thr His Xaa Ala Thr Leu Val
9666  145             150             155             160
9667  Thr Leu Gly Asp Phe Gly Asp Pro His Val Leu Leu Gly Val Val Gly
9668              165             170             175
9669  Ile Ile Leu Thr Phe Ala Leu Tyr Thr Leu Lys Ile Arg Gly Ser Phe
9670              180             185             190
9671  Ile Ile Ala Val Leu Ile Thr Ser Ile Leu Ala Trp Val Leu Lys Leu
9672          195             200             205
9673  Ala Pro Tyr Pro Ser Glu Phe Phe Ser Met Pro Ala Ser Ile Gly Pro
9674      210             215             220
9675  Ile Ala Phe Gln Leu Asp Phe Lys Gly Ile Phe Phe Asp Ala Ser Gly
9676  225             230             235             240
9677  Ala Phe Thr Leu Ala Leu Val Pro Val Ile Ile Thr Phe Phe Val Thr
9678              245             250             255
9679  Asp Leu Phe Asp Ser Leu Gly Thr Leu Ala Gly Ile Gly His Lys Thr
9680              260             265             270
9681  Asp Phe Phe Asn Asp Glu Glu Lys Asn Lys Glu Leu Glu Lys Thr Leu
9682          275             280             285
9683  Glu Ala Asp Ala Val Ala Ser Leu Gly Ser Ala Val Val Gly Val Ser
9684          290             295             300
9685  Thr Thr Thr Ala Phe Ile Glu Ser Ala Ser Gly Val Glu Glu Gly Gly
9686  305             310             315             320
```

E--> 9665 (annotation beside lines: circled "146"; circled "Xaa"; handwritten "see item 9")

```
9687  Arg Thr Gly Leu Thr Ala Val Phe Thr Gly Leu Phe Phe Val Leu Thr
9688              325             330             335
9689  Leu Phe Cys Leu Pro Leu Leu Lys Ala Ile Pro Ser Asn Ala Ile Tyr
9690              340             345             350
9691  Pro Val Leu Val Val Val Gly Val Leu Met Phe Ser Val Leu Glu Gly
9692              355             360             365
9693  Val Asn Phe Lys Asp Met Ala Ile Ser Val Ser Thr Phe Leu Thr Val
9694          370             375             380
9695  Val Met Met Pro Leu Thr Phe Ser Ile Ala Asp Gly Leu Ala Phe Gly
9696  385             390             395                 400
9697  Phe Leu Ser Tyr Ser Ile Ile Lys Leu Val Gln Lys Asp Phe Lys Ala
9698              405             410                 415
9699  Leu Asn Ser Gly Ile Ile Ile Leu Cys Ile Ile Ser Val Ser Val Phe
9700              420             425                 430
9701  Ile Phe Arg
9702          435
16782 <210> SEQ ID NO: 246
16783 <211> LENGTH: 1185
16784 <212> TYPE: PRT
16785 <213> ORGANISM: Helicobacter pylori
16787 <400> SEQUENCE: 246
16788  Met Gln Lys Ile Ile Asp Asp Ser Leu Glu Leu Ala Lys Lys Leu Gln
16789  1               5               10                  15
16790  Asp Ser Ile Ser Asn His Leu Ser Asp Gln Glu Lys Ala Phe His Ser
16791              20              25              30
16792  Lys Met Gln Lys Leu Leu Asn Asn Pro Glu Asn Lys Val Met Leu Ile
16793          35              40              45
16794  Glu Leu Met Asp Arg Ser Phe Arg Cys Leu Asp Asn Lys Ala Arg Phe
16795      50              55              60
16796  Glu Met Ile Glu His Val Leu Asp Lys Tyr Lys Ser Arg Glu Ile Phe
16797  65              70              75                  80
16798  Ser Pro Phe Glu Lys Val Leu Leu Met Gly Phe Leu Ser Phe Gly Lys
16799              85              90                  95
16800  Met Leu Pro Asp Met Ser Val Pro Phe Phe Val Asn Lys Ile Arg Ser
16801              100             105                 110
16802  Asp Thr Lys Ala Met Val Leu Asp Gln Glu Glu Ser Gln Leu Lys Glu
16803          115             120             125
16804  Arg Ile Leu Lys Arg Lys Asn Glu Lys Ile Ile Leu Asn Val Asn Phe
16805      130             135             140
16806  Ile Gly Glu Glu Val Leu Gly Glu Glu Glu Ala Asn Ala Arg Phe Glu
16807  145             150             155                 160
16808  Lys Tyr Ser Gln Ala Leu Lys Ser Asn Tyr Ile Gln Tyr Ile Ser Ile
16809              165             170                 175
16810  Lys Ile Thr Thr Ile Phe Ser Gln Ile Asn Ile Leu Asp Phe Glu Tyr
16811          180             185             190
16812  Ser Lys Lys Glu Ile Val Lys Arg Leu Asp Ala Leu Tyr Ala Leu Ala
16813          195             200             205
16814  Leu Glu Glu Glu Lys Lys Gln Gly Met Pro Lys Phe Ile Asn Leu Asp
16815      210             215             220
```

```
16816  Met Glu Glu Phe Arg Asp Leu Glu Leu Thr Val Glu Ser Phe Met Glu
16817  225                 230             235                 240
16818  Ser Ile Ala Lys Phe Asp Leu Asn Ala Gly Ile Val Leu Gln Ala Tyr
16819                  245             250                 255
16820  Ile Pro Asp Ser Tyr Glu Tyr Leu Lys Lys Leu His Ala Phe Ser Lys
16821              260             265                 270
16822  Glu Arg Val Leu Lys Gly Leu Lys Pro Ile Lys Ile Arg Phe Val Lys
16823          275                 280                 285
16824  Gly Ala Asn Met Glu Ser Glu Glu Thr Ile Ala Ser Val Lys Asp Trp
16825      290                 295                 300
16826  Ala Leu Pro Thr Phe Ser Asn Lys Gln Asp Thr Asp Ser Asn Tyr Asn
16827  305                 310                 315                 320
16828  Lys Met Leu Asp Phe Val Leu Glu Gly Asp Asn Tyr Lys Tyr Ile His
16829                  325                 330                 335
16830  Ile Gly Ala Ala Ser His Asn Ile Phe Glu Ile Ala Tyr Val Tyr Thr
16831              340                 345                 350
16832  Arg Ile His Ala Ile Asn Asp Pro Val Val Leu Glu His Phe Ser Phe
16833          355                 360                 365
16834  Glu Met Leu Glu Gly Met Ser Leu Gln Ala Ser Gln Glu Leu Lys Glu
16835      370                 375                 380
16836  Met His Lys Leu Ile Leu Tyr Ala Pro Val Cys Asp Glu Ala His Phe
16837  385                 390                 395                 400
16838  Asn Asn Ala Ile Ala Tyr Leu Val Arg Arg Leu Asp Glu Asn Thr Ser
16839                  405                 410                 415
16840  Ser Asp Asn Phe Met Lys Ala Phe Phe Asn Leu Lys Val Gly Thr Ser
16841              420                 425                 430
16842  Glu Trp Lys Asp Gln Glu Gln Arg Phe Leu Asn Ser Leu Lys Gly Ile
16843          435                 440                 445
16844  Ala Thr Leu Asp Asn Ala Thr His Arg Thr Gln Asp Arg Asn Ala Lys
16845      450                 455                 460
16846  Gln Ser Gly His Thr Thr Tyr Pro Asn His Ser Phe Lys Asn Glu Ser
16847  465                 470                 475                 480
16848  Asp Thr Asp Phe Ile Leu Lys Ala Asn Arg Glu Trp Ala Lys Lys Val
16849              485                 490                 495
16850  Arg Glu Lys Met Arg Asn Ala Pro Ile Leu Glu Leu Tyr Pro Glu Met
16851              500                 505                 510
16852  Asp Gly Arg Phe Glu Asp Pro Asn Leu Thr Pro Leu Glu Val Phe Asp
16853          515                 520                 525
16854  Arg Ile His His Lys Lys Ile Ala Ser Val His Leu Ala Asp Lys Glu
16855          530                 535                 540
16856  Ala Ile Leu Lys Ala Leu Glu Val Ala Lys Ser Asp Lys Ser Arg Phe
16857  545                 550                 555                 560
16858  Ser Gln Lys Ser Phe Thr Glu Ile His Ala Leu Met Ser Gln Thr Ala
16859                  565                 570                 575
16860  Gln Leu Phe Arg Glu Arg Arg Gly Asp Leu Ile Gly Ile Ser Ala Leu
16861              580                 585                 590
16862  Glu Val Gly Lys Thr Phe Ala Glu Thr Asp Ala Glu Val Ser Glu Ala
16863          595                 600                 605
16864  Ile Asp Phe Leu Glu Phe Tyr Pro Tyr Ser Leu Arg Val Leu Gln Glu
```

```
16865        610                  615                  620
16866   Gln Asn Thr Lys Thr Gln Phe Thr Pro Lys Gly Val Gly Val Val Ile
16867   625                  630                  635                  640
16868   Ala Pro Trp Asn Phe Pro Val Gly Ile Ser Val Gly Thr Ile Ala Ala
16869                  645                  650                  655
16870   Pro Leu Ala Thr Gly Asn Arg Val Ile Tyr Lys Pro Ser Ser Leu Ser
16871                  660                  665                  670
16872   Ser Val Thr Gly Tyr Lys Leu Cys Glu Cys Phe Trp Asp Ala Gly Val
16873                  675                  680                  685
16874   Pro Arg Asp Ala Leu Ile Tyr Leu Pro Ser Lys Gly Ser Asp Ile Ser
16875                  690                  695                  700
16876   Glu His Leu Leu Arg Asp Glu Ser Ile Gln Phe Ala Ile Leu Thr Gly
16877   705                  710                  715                  720
16878   Gly Glu Asp Thr Ala Tyr Lys Met Leu Lys Ala Asn Pro Thr Leu Ala
16879                  725                  730                  735
16880   Leu Ser Ala Glu Thr Gly Gly Lys Asn Ala Thr Ile Val Ser Lys Met
16881                  740                  745                  750
16882   Ala Asp Arg Asp Gln Ala Ile Lys Asn Val Ile His Ser Ala Phe Ser
16883                  755                  760                  765
16884   Asn Ser Gly Gln Lys Cys Ser Ala Thr Ser Leu Leu Val Leu Glu Lys
16885                  770                  775                  780
16886   Glu Val Tyr Glu Asp Glu Asn Phe Lys Lys Thr Leu Ile Asp Ala Thr
16887   785                  790                  795                  800
16888   Leu Ser Leu Ser Val Gly Asp Pro Phe Asp Phe Lys Asn Lys Ile Gly
16889                  805                  810                  815
16890   Ala Leu Ala Asp Lys Pro Asn Glu Lys Val Ile Lys Ala Ile Asp Glu
16891                  820                  825                  830
16892   Leu Lys Ser Tyr Glu Asn Tyr Glu Ile Pro Val Ser Phe Val Asn Asp
16893                  835                  840                  845
16894   Asn Pro Tyr Leu Met Lys Pro Ser Ile Lys Tyr Gly Thr Lys Lys Gly
16895                  850                  855                  860
16896   Asp Phe Thr His Gln Thr Glu Leu Phe Thr Pro Ile Leu Ser Val Met
16897   865                  870                  875                  880
16898   Glu Ala Lys Asp Leu Asp Glu Ala Ile Glu Ile Ala Asn Ser Thr Gly
16899                  885                  890                  895
16900   Tyr Gly Leu Thr Ser Ala Leu Glu Ser Leu Asp Glu Arg Glu Trp Glu
16901                  900                  905                  910
16902   Tyr Tyr Leu Glu Arg Ile Glu Ala Gly Asn Ile Tyr Ile Asn Lys Pro
16903                  915                  920                  925
16904   Thr Thr Gly Ala Ile Val Leu Arg Gln Pro Phe Gly Gly Val Lys Lys
16905                  930                  935                  940
16906   Ser Ala Val Gly Phe Gly Arg Lys Val Gly Ile Phe Asn Tyr Ile Thr
16907   945                  950                  955                  960
16908   Gln Phe Val Asn Ile Cys Gln Glu Glu Glu Asp Glu Asn Ala Leu Lys
16909                  965                  970                  975
16910   Asn Pro Leu Ser Glu Ala Leu Glu Asn Leu Thr Gln Lys Gly Tyr Asp
16911                  980                  985                  990
16912   Glu His Thr His Glu Leu Lys Arg Ala Ile Phe Met Ala Lys Ser Tyr
16913                  995                  1000                 1005
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RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,913   TIME: 13:45:02

Input Set : A:\06132.013001.seqlist.txt
Output Set: N:\CRF3\07232001\I895913.raw

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        16914  Ala Tyr His Tyr Lys His Glu Phe Ser Gln Thr Lys Asp Tyr Val Lys
        16915        1010            1015            1020
        16916  Ile Arg Gly Glu Asp Asn Leu Phe Ser Tyr Thr Lys Val Lys Ser Val
E-->    16917  1025            1030            1035            (104)
        16918  Gly Tyr Arg Ile Thr Glu Lys Asp Thr Leu Ser Asp Met Leu Gly Val
        16919            1045            1050            1055
        16920  Ala Leu Ala Cys Leu Ile Ser Gln Ile Pro Leu Thr Leu Ser Ile Glu
        16921        1060            1065            1070
        16922  Asn Glu Arg Thr Asn Lys Asp Leu Thr Phe Phe Leu Glu Cys Leu Lys
        16923        1075            1080            1085
        16924  Ala Leu Gln Ala Ser Ala Pro Ile Val Tyr Glu Ser Leu Gln Lys Phe
        16925        1090            1095            1100
        16926  Ser Glu Lys Leu Asn Thr Phe Asn Arg Val Arg Tyr Leu Lys Ser Asp
E-->    16927  1105            1110            1115            (112)
        16928  Leu Asp Leu Leu His Glu Gln Ala Ser Ala Leu Gly Met Val Leu Ala
        16929            1125            1130            1135
        16930  Thr Ala Lys Pro Cys Leu Asn Gly Arg Phe Glu Leu Leu Tyr Tyr His
        16931            1140            1145            1150
        16932  Leu Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly
        16933        1155            1160            1165
        16934  Ser Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu
        16935        1170            1175            1180
        16936  Lys
        16937  1185
        21547  <210> SEQ ID NO: 318
        21548  <211> LENGTH: 291
        21549  <212> TYPE: PRT
        21550  <213> ORGANISM: Helicobacter pylori
        21552  <400> SEQUENCE: 318
        21553  Lys Asn Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp
        21554  1               5               10              15
E-->    21555  Lys Leu Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala
        21556            20              25              30
        21557  Glu Gln His Ala Leu Thr Ser Ser Ser Ala Met Ala Lys Glu Gly Phe
        21558            35              40              45
        21559  Lys Pro Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp
        21560        50              55              60
        21561  Ser Ile Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala
        21562  65              70              75              80
        21563  Ile Asp Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly
        21564            85              90              95
        21565  Leu Leu Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe
        21566            100             105             110
        21567  Ala Pro Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn
        21568            115             120             125
        21569  Glu His Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe
        21570        130             135             140
        21571  Ala Leu Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln
        21572  145             150             155             160
```

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21573   Ser Glu Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly
21574                   165             170             175
21575   Asn Gly Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys
21576               180             185             190
21577   Asn Ile Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp
21578           195             200             205
21579   Pro Asn Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe
21580       210             215             220
21581   Ser Asp Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe
21582   225             230             235             240
21583   Leu Ser Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile
21584               245             250             255
21585   Asp Glu Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu
21586               260             265             270
21587   Gly Leu Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly
21588           275             280             285
21589   Gln Glu Arg
21590       290
24908 <210> SEQ ID NO: 362
24909 <211> LENGTH: 226
24910 <212> TYPE: PRT
24911 <213> ORGANISM: Helicobacter pylori
24913 <400> SEQUENCE: 362
24914   Met Gln Phe Thr Gly Lys Asn Val Leu Ile Thr Gly Ala Ser Lys Gly
24915   1               5               10              15
24916   Ile Gly Ala Glu Ile Ala Lys Thr Leu Ala Ser Met Gly Leu Lys Val
24917               20              25              30
24918   Trp Ile Asn Tyr Arg Ser Asn Ala Glu Val Ala Asp Ala Leu Lys Asn
24919           35              40              45
24920   Glu Leu Glu Glu Lys Gly Tyr Lys Ala Ala Val Ile Lys Phe Asp Ala
24921       50              55              60
24922   Ala Ser Glu Ser Asp Phe Ile Glu Ala Ile Gln Thr Ile Val Gln Ser
24923   65              70              75              80
24924   Asp Gly Gly Leu Ser Tyr Leu Val Asn Asn Ala Gly Val Val Arg Asp
24925               85              90              95
24926   Lys Leu Ala Ile Lys Met Lys Thr Glu Asp Phe His His Val Ile Asp
24927               100             105             110
24928   Asn Asn Leu Thr Ser Ala Phe Ile Gly Cys Arg Glu Ala Leu Lys Val
24929           115             120             125
24930   Met Ser Lys Ser Arg Phe Gly Ser Val Val Asn Val Ala Ser Ile Ile
24931       130             135             140
24932   Gly Glu Arg Gly Asn Met Gly Gln Thr Asn Tyr Ser Ala Ser Lys Gly
24933   145             150             155             160
24934   Gly Met Ile Ala Met Ser Lys Ser Phe Ala Tyr Glu Gly Ala Leu Arg
24935               165             170             175
24936   Asn Ile Arg Phe Asn Ser Val Thr Pro Gly Phe Ile Glu Thr Asp Met
24937               180             185             190
24938   Asn Ala Asn Leu Lys Asp Glu Leu Lys Ala Asp Tyr Val Lys Asn Ile
24939           195             200             205
```

RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,913 TIME: 13:45:04

Input Set : A:\06132.013001.seqlist.txt
Output Set: N:\CRF3\07232001\I895913.raw

E--> 24940 Pro Leu Asn Arg Leu Gly Ser Ala Lys Glu Val Ala Glu Ala Val Xaa item 9
  24941   210   215   220
  24942 Phe Phe
  24943 225

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 07/23/2001
PATENT APPLICATION: **US/09/895,913**   TIME: 13:45:05

Input Set : **A:\06132.013001.seqlist.txt**
Output Set: **N:\CRF3\07232001\I895913.raw**

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1296 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:1457 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:1457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1491 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:2729 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:2729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:2730 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:2730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:2815 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:3105 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:41
L:3105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:4186 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:59
L:4186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:5447 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:85
L:5447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85
L:9567 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:145
L:9567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145
L:9665 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:146
L:16738 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:245
L:16758 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:245
L:16778 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:245
L:16917 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:246
M:332 Repeated in SeqNo=246
L:21079 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:307
L:21079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:307
L:21476 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:317
L:21476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:317
L:21477 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:317
L:21477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:317
L:21555 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:318
L:24902 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:361
L:24902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:361
L:24903 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:361
L:24903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:361
L:24940 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:362